



SEQUENCE LISTING

<110> CNRS

<120> RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN IMMUNE RESPONSES

<130> 1721-47

<140> 10/048,116
<141> 2002-02-27<150> PCT/FR00/02193
<151> 2000-07-28<150> FR99/09862
<151> 1999-07-29

<160> 8

<170> PatentIn Ver. 2.0

<210> 1

<211> 1517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: construct coding IAalpha(d)/Fc

<220>

<221> CDS

<222> (18)..(1502)

<400> 1

aaaggggggg attcagg atg ccg tgc agc aga gct ctg att ctg ggg gtc 50
Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
1 5 10ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att 98
Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Glu Asp Asp Ile
15 20 25gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct 146
Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
30 35 40gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc 194
Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
45 50 55tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt 242
Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
60 65 70 75

ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct		290	
Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala			
80	85	90	
gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc		338	
Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr			
95	100	105	
cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct		386	
Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro			
110	115	120	
gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc		434	
Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile			
125	130	135	
ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc		482	
Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val			
140	145	150	155
aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc		530	
Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser			
160	165	170	
ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att		578	
Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile			
175	180	185	
tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa		626	
Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys			
190	195	200	
cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act		674	
His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr			
205	210	215	
gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag		722	
Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu			
220	225	230	235
ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttg caa		770	
Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln			
240	245	250	
gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc		818	
Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro			
255	260	265	
aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg		866	
Thr Ile Lys Pro Cys Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu			
270	275	280	
ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc		914	
Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu			
285	290	295	
atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gat gtg agc		962	

Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser					
300	305	310	315		
gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa					1010
Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu					
320		325	330		
gta cac aca gct cag aca caa acc cat aga gag gat tac aac agt act					1058
Val His Thr Ala Gln Thr Gln His Arg Glu Asp Tyr Asn Ser Thr					
335	340	345			
ctc cggt gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt					1106
Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser					
350	355	360			
ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc					1154
Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro					
365	370	375			
atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag					1202
Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln					
380	385	390	395		
gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc					1250
Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val					
400	405	410			
act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg					1298
Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val					
415	420	425			
gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac act gaa					1346
Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu					
430	435	440			
cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag ctg aga					1394
Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg					
445	450	455			
gtg gaa aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg					1442
Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val					
460	465	470	475		
gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg					1490
Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg					
480	485	490			
act ccg ggt aaa tgatgactcg acctg					1517
Thr Pro Gly Lys					
495					

<210> 2
 <211> 495
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: construct
coding IAalpha(d)/Fc

<400> 2
Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
1 5 10 15

Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
20 25 30

Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
35 40 45

Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
50 55 60

Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
65 70 75 80

Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
85 90 95

Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
100 105 110

Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
115 120 125

Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
130 135 140

Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
145 150 155 160

Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
165 170 175

Tyr Leu Thr Phe Ile Pro Ser Asp Asp Ile Tyr Asp Cys Lys Val
180 185 190

Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
195 200 205

Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Ser
210 215 220

Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
225 230 235 240

Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
245 250 255

Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
260 265 270

Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val

275	280	285
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser		
290	295	300
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp		
305	310	315
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln		
325	330	335
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser		
340	345	350
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys		
355	360	365
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile		
370	375	380
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro		
385	390	395
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met		
405	410	415
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn		
420	425	430
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser		
435	440	445
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn		
450	455	460
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu		
465	470	475
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys		
485	490	495
<210> 3		
<211> 1485		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence:coding region		
of SEQ ID NO:1		
<220>		
<221> CDS		
<222> (1)..(1485)		
<400> 3		
atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc 48		

Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr				
1	5	10	15	
atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta				96
Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val				
20	25	30		
ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag				144
Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln				
35	40	45		
tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat				192
Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp				
50	55	60		
aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc				240
Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu				
65	70	75	80	
ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac				288
Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn				
85	90	95		
ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag				336
Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu				
100	105	110		
gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag				384
Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln				
115	120	125		
ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc				432
Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile				
130	135	140		
aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat				480
Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr				
145	150	155	160	
gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct				528
Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser				
165	170	175		
tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg				576
Tyr Leu Thr Phe Ile Pro Ser Asp Asp Ile Tyr Asp Cys Lys Val				
180	185	190		
gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag				624
Glu His Trp Gly Leu Glu Pro Val Leu Lys His Trp Glu Pro Glu				
195	200	205		
att cca gcc ccc atg tca gag ctg aca gaa act gga ggt gga gga tcc				672
Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Ser				
210	215	220		
act aca gct cca tca gct cag ctc gaa aaa gag ctc cag gcc ctg gag				720
Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu				

225	230	235	240	
aag gaa aat gca cag ctg gaa tgg gag ttg caa gca ctg gaa aag gaa Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu 245		250		768
		255		
ctg gct cag gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys 260		265		816
		270		
cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val 275		280		864
		285		
ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser 290		295		912
		300		
ccc ata gtc aca tgt gtg gtg gat gtg agc gag gat gac cca gat Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp 305		310		960
		315		
		320		
gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln 325		330		1008
		335		
aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser 340		345		1056
		350		
gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys 355		360		1104
		365		
tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile 370		375		1152
		380		
tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro 385		390		1200
		395		
		400		
cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg Pro Pro Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met 405		410		1248
		415		
gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn 420		425		1296
		430		
ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser 435		440		1344
		445		
gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn 450		455		1392
		460		

tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg 1440
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
465 470 475 480

cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aaa 1485
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
485 490 495

<210> 4
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:coding region
of SEQ ID NO:1

<400> 4
Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
1 5 10 15

Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
20 25 30

Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
35 40 45

Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
50 55 60

Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
65 70 75 80

Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
85 90 95

Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
100 105 110

Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
115 120 125

Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
130 135 140

Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
145 150 155 160

Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
165 170 175

Tyr Leu Thr Phe Ile Pro Ser Asp Asp Ile Tyr Asp Cys Lys Val
180 185 190

Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
195 200 205

Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Ser
210 215 220

Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
225 230 235 240

Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
245 250 255

Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
260 265 270

Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
275 280 285

Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
290 295 300

Pro Ile Val Thr Cys Val Val Asp Val Ser Glu Asp Asp Pro Asp
305 310 315 320

Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
325 330 335

Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
340 345 350

Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
355 360 365

Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
370 375 380

Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
385 390 395 400

Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
405 410 415

Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
420 425 430

Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
435 440 445

Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
450 455 460

Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
465 470 475 480

His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
485 490 495

<210> 5
 <211> 951
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:construct
 coding LACK/I-Abeta(d)/leucine zipper

<220>
 <221> CDS
 <222> (21)...(938)

<400> 5
 aaagggggga attcttagag atg gct ctg cag atc ccc agc ctc ctc ctc tca 53
 Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser
 1 5 10

gct gct gtg gtg ctg atg gtg ctg agc agc ccc ggg act gag ggc 101
 Ala Ala Val Val Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly
 15 20 25

gga aac tcc atc tgc ttc tcg ccg tcg ctg gag cac ccg atc gtg gtg 149
 Gly Asn Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Val Val
 30 35 40

tcc ggc agc tgg gac gga ggt ggg ggc tca cta gtg ccc cga ggc tct 197
 Ser Gly Ser Trp Asp Gly Gly Ser Leu Val Pro Arg Gly Ser
 45 50 55

gga ggt gga ggc tcc gaa agg cat ttc gtg gtc cag ttc aag ggc gag 245
 Gly Gly Gly Ser Glu Arg His Phe Val Val Gln Phe Lys Gly Glu
 60 65 70 75

tgc tac tac acc aac ggg acg cag cgc ata cgg ctc gtg acc aga tac 293
 Cys Tyr Tyr Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr
 80 85 90

atc tac aac cgg gag gag tac gtg cgc tac gac agc gac gtg ggc gag 341
 Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu
 95 100 105

tac cgc gcg gtg acc gag ctg ggg cgg cca gac gcc gag tac tgg aac 389
 Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn
 110 115 120

agc cag ccg gag atc ctg gag cga acg cgg gcc gag gtg gac acg gcg 437
 Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala
 125 130 135

tgc aga cac aac tac gag ggg cgg gag acc agc acc tcc ctg cgg cgg 485
 Cys Arg His Asn Tyr Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg
 140 145 150 155

ctt gaa cag ccc aat gtc gcc atc tcc ctg tcc agg aca gag gcc ctc 533

Leu	Glu	Gln	Pro	Asn	Val	Ala	Ile	Ser	Leu	Ser	Arg	Thr	Glu	Ala	Leu	
160									165						170	
aac	cac	cac	aac	act	ctg	gtc	tgt	tcg	gtg	aca	gat	ttc	tac	cca	gcc	581
Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	Thr	Asp	Phe	Tyr	Pro	Ala	
175								180						185		
aag	atc	aaa	gtg	cgc	tgg	tcc	agg	aat	ggc	cag	gag	gag	aca	gtg	ggg	629
Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	Gln	Glu	Glu	Thr	Val	Gly	
190							195				200					
gtc	tca	tcc	aca	cag	ctt	att	agg	aat	ggg	gac	tgg	acc	ttc	cag	gtc	677
Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	Asp	Trp	Thr	Phe	Gln	Val	
205						210						215				
ctg	gtc	atg	ctg	gag	atg	acc	cct	cat	cag	gga	gag	gtc	tac	acc	tgc	725
Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His	Gln	Gly	Glu	Val	Tyr	Thr	Cys	
220						225				230				235		
cat	gtg	gag	cat	ccc	agc	ctg	aag	agc	ccc	atc	act	gtg	gag	tgg	agg	773
His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	Ile	Thr	Val	Glu	Trp	Arg	
						240				245				250		
gca	cag	tcc	gag	tct	gcc	cgg	agc	aag	gga	ggt	gga	gga	tcc	act	aca	821
Ala	Gln	Ser	Glu	Ser	Ala	Arg	Ser	Lys	Gly	Gly	Gly	Gly	Ser	Thr	Thr	
						255			260				265			
gct	cca	tca	gct	cag	ttg	aaa	aag	aaa	ttg	caa	gca	ctg	aag	aaa	aag	869
Ala	Pro	Ser	Ala	Gln	Leu	Lys	Lys	Lys	Leu	Gln	Ala	Leu	Lys	Lys	Lys	
						270			275				280			
aac	gct	cag	ctg	aag	tgg	aaa	ctt	caa	gcc	ctc	aag	aag	aaa	ctc	gcc	917
Asn	Ala	Gln	Leu	Lys	Trp	Lys	Leu	Gln	Ala	Leu	Lys	Lys	Lys	Lys	Leu	Ala
						285			290				295			
cag	cat	cat	cat	cat	cat	cat	tgagtgcacc	tgc								951
Gln	His	His	His	His	His	His										
						300			305							

<210> 6
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:construct
coding LACK/I-Abeta(d)/leucine zipper

<400> 6
Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val Val
1 5 10 15

Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly Gly Asn Ser Ile Cys
20 25 30

Phe Ser Pro Ser Leu Glu His Pro Ile Val Val Ser Gly Ser Trp Asp
35 40 45

Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Ser
50 55 60

Glu Arg His Phe Val Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn
65 70 75 80

Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu
85 90 95

Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
100 105 110

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile
115 120 125

Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr
130 135 140

Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn
145 150 155 160

Val Ala Ile Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr
165 170 175

Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg
180 185 190

Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln
195 200 205

Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu
210 215 220

Met Thr Pro His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro
225 230 235 240

Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser
245 250 255

Ala Arg Ser Lys Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln
260 265 270

Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys
275 280 285

Trp Lys Leu Gln Ala Leu Lys Lys Leu Ala Gln His His His His
290 295 300

His His
305

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<212> DNA
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Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val Val	
1 5 10 15	
ctg atg gtg ctg agc agc ccc ggg act gag ggc gga aac tcc atc tgc	96
Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly Gly Asn Ser Ile Cys	
20 25 30	
ttc tcg ccg tcg ctg gag cac ccg atc gtg gtg tcc ggc agc tgg gac	144
Phe Ser Pro Ser Leu Glu His Pro Ile Val Val Ser Gly Ser Trp Asp	
35 40 45	
gga ggt ggg ggc tca cta gtg ccc cga ggc tct gga ggt gga ggc tcc	192
Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Ser	
50 55 60	
gaa agg cat ttc gtg gtc cag ttc aag ggc gag tgc tac tac acc aac	240
Glu Arg His Phe Val Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn	
65 70 75 80	
ggg acg cag cgc ata cgg ctc gtg acc aga tac atc tac aac cgg gag	288
Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu	
85 90 95	
gag tac gtg cgc tac gac gac gtg ggc gag tac cgc gcg gtg acc	336
Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr	
100 105 110	
gag ctg ggg cgg cca gac gcc gag tac tgg aac agc cag ccg gag atc	384
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile	
115 120 125	
ctg gag cga acg cgg gcc gag gtg gac acg gcg tgc aga cac aac tac	432
Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr	
130 135 140	
gag ggg ccg gag acc agc acc tcc ctg cgg cgg ctt gaa cag ccc aat	480
Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn	
145 150 155 160	
gtc gcc atc tcc ctg tcc agg aca gag gcc ctc aac cac cac aac act	528
Val Ala Ile Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr	
165 170 175	
ctg gtc tgt tcg gtg aca gat ttc tac cca gcc aag atc aaa gtg cgc	576

Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg			
180	185	190	
tgg ttc agg aat ggc cag gag gag aca gtg ggg gtc tca tcc aca cag			624
Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln			
195	200	205	
ctt att agg aat ggg gac tgg acc ttc cag gtc ctg gtc atg ctg gag			672
Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu			
210	215	220	
atg acc cct cat cag gga gag gtc tac acc tgc cat gtg gag cat ccc			720
Met Thr Pro His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro			
225	230	235	240
agc ctg aag agc ccc atc act gtg gag tgg agg gca cag tcc gag tct			768
Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser			
245	250	255	
gcc cg ^g agc aag gga ggt gga gga tcc act aca gct cca tca gct cag			816
Ala Arg Ser Lys Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln			
260	265	270	
ttg aaa aag aaa ttg caa gca ctg aag aaa aag aac gct cag ctg aag			864
Leu Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys			
275	280	285	
tgg aaa ctt caa gcc ctc aag aag aaa ctc gcc cag cat cat cat cat			912
Trp Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln His His His			
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cat cat			918
His His			
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<211> 306
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:coding seq of
SEQ ID NO:5

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Phe Ser Pro Ser Leu Glu His Pro Ile Val Val Ser Gly Ser Trp Asp
35 40 45

Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Ser

50	55	60
Glu Arg His Phe Val Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn		
65	70	75
80		
Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu		
85	90	95
Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr		
100	105	110
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile		
115	120	125
Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr		
130	135	140
Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn		
145	150	155
160		
Val Ala Ile Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr		
165	170	175
Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg		
180	185	190
Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln		
195	200	205
Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu		
210	215	220
Met Thr Pro His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro		
225	230	235
240		
Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser		
245	250	255
Ala Arg Ser Lys Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln		
260	265	270
Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys		
275	280	285
Trp Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln His His His		
290	295	300
His His		
305		